

Abstract

The present invention relates to a versatile method of identifying genes having invariant peptides as functional signatures in a genome especially in SARS using software GeneDecipher, said method comprising steps of generating peptide libraries from the known genomes with peptide of length 'N' computationally arranged in an alphabetical order, artificially translating the test genome to obtain peptide, identifying the reading frames in the peptide on the basis of overlappings with the peptide libraries, converting each peptide sequence into an alphanumeric sequence with one corresponding to each reading frame, training Artificial Neural Network (ANN) with sigmoidal learning function to the alphanumeric sequence, deciphering the protein coding regions in the test genome, thus, identifying invariant peptides serving as functional signatures, also, four novel genes of SARS and their corresponding proteins, lastly, a method of drug target development in the management in a disease condition